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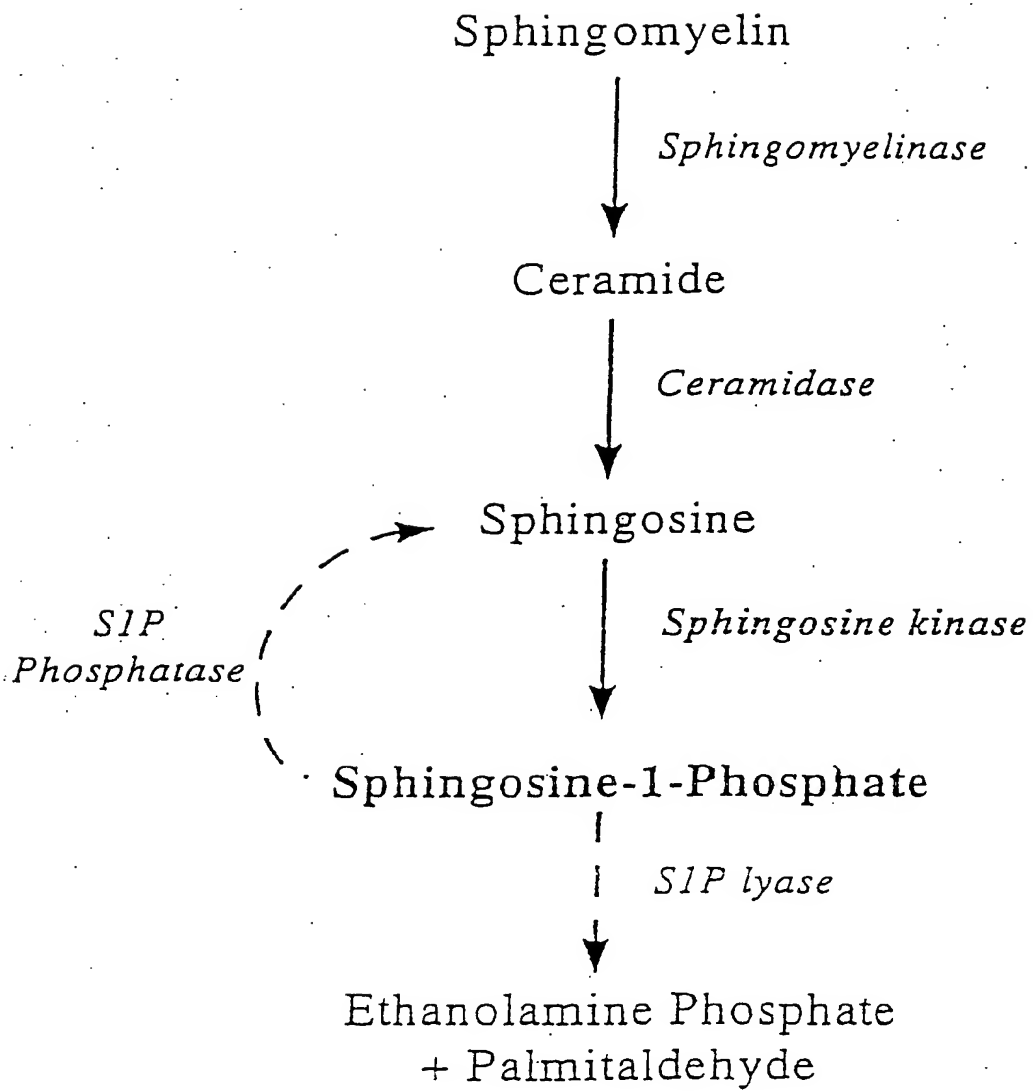


Figure 1

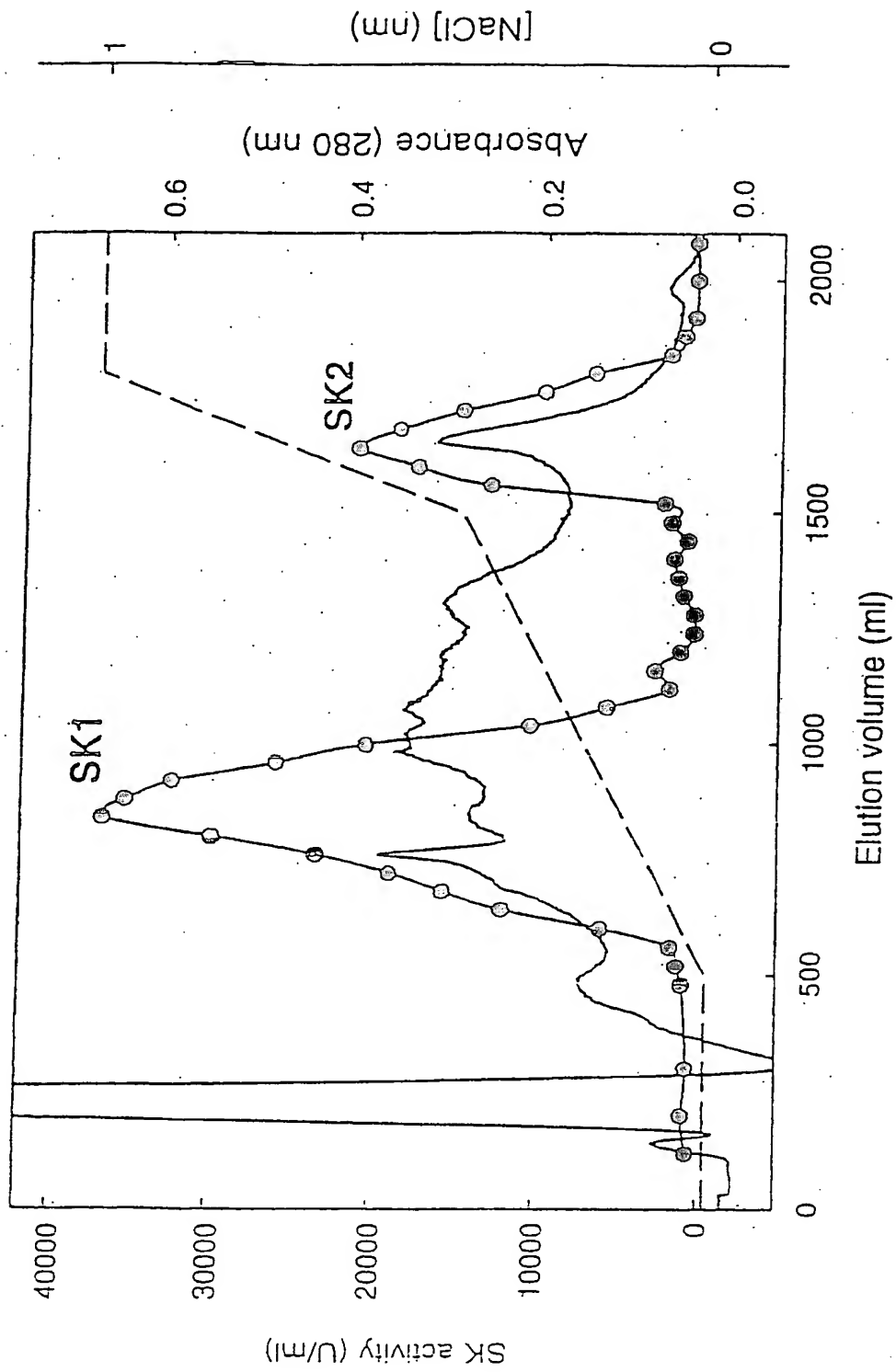
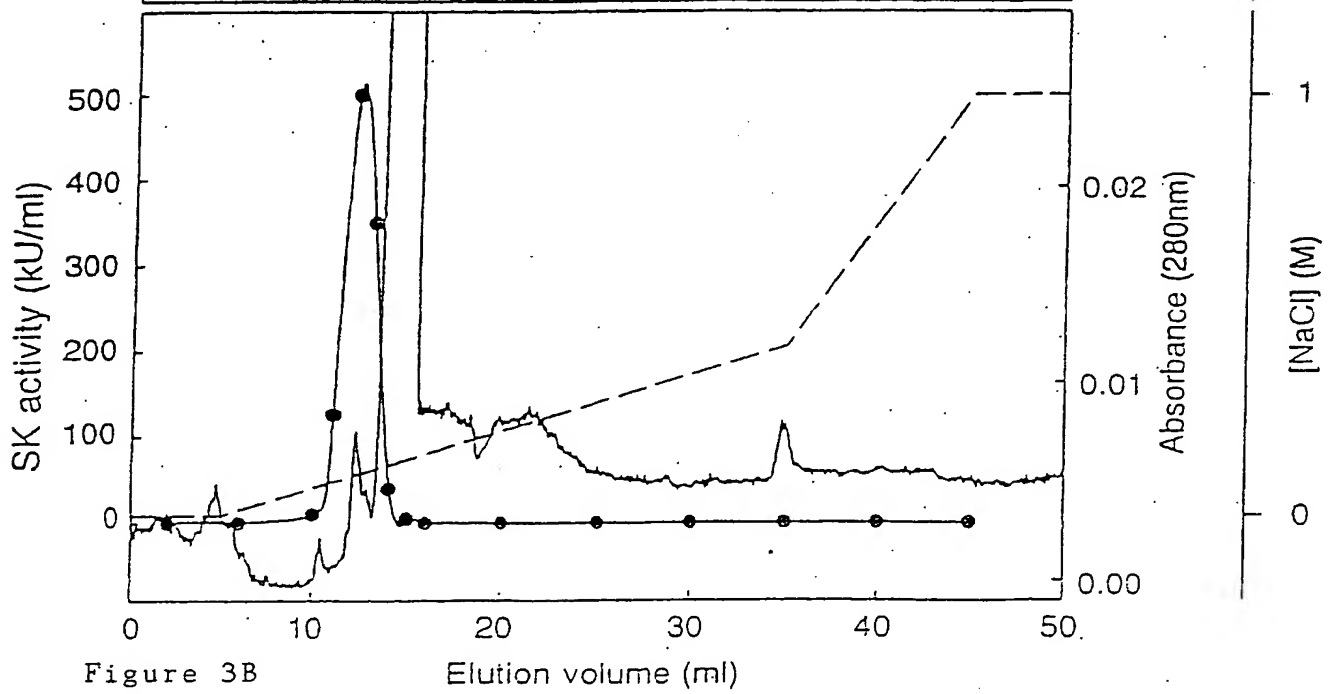
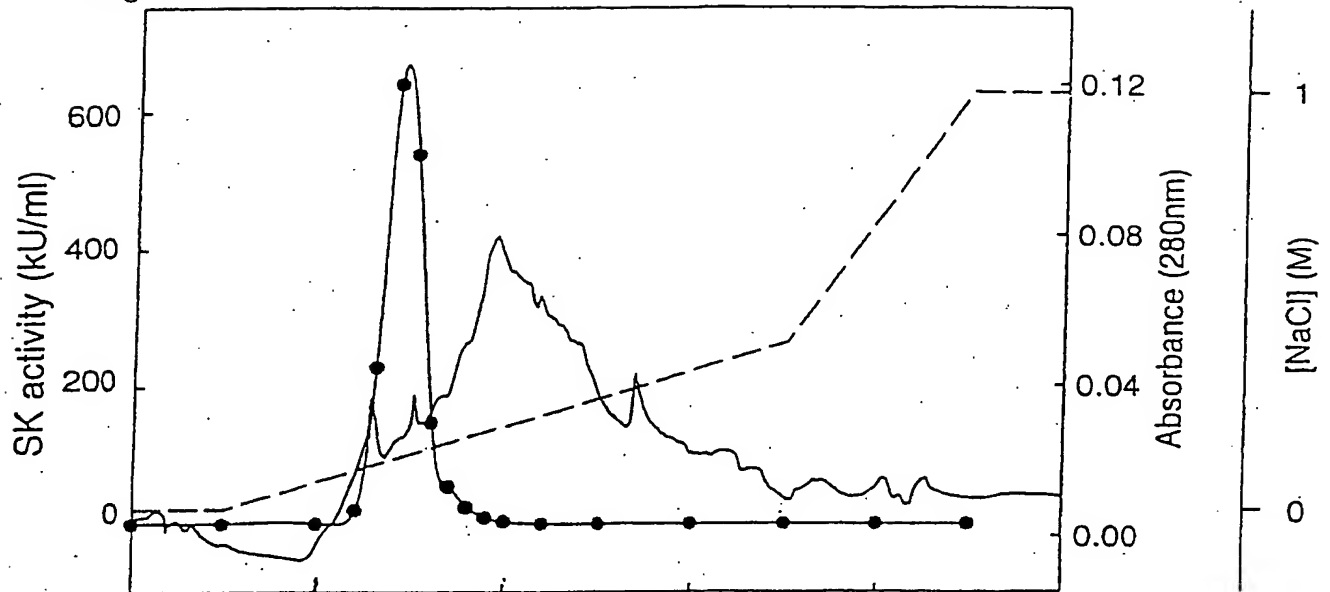


Figure 2

Figure 3A



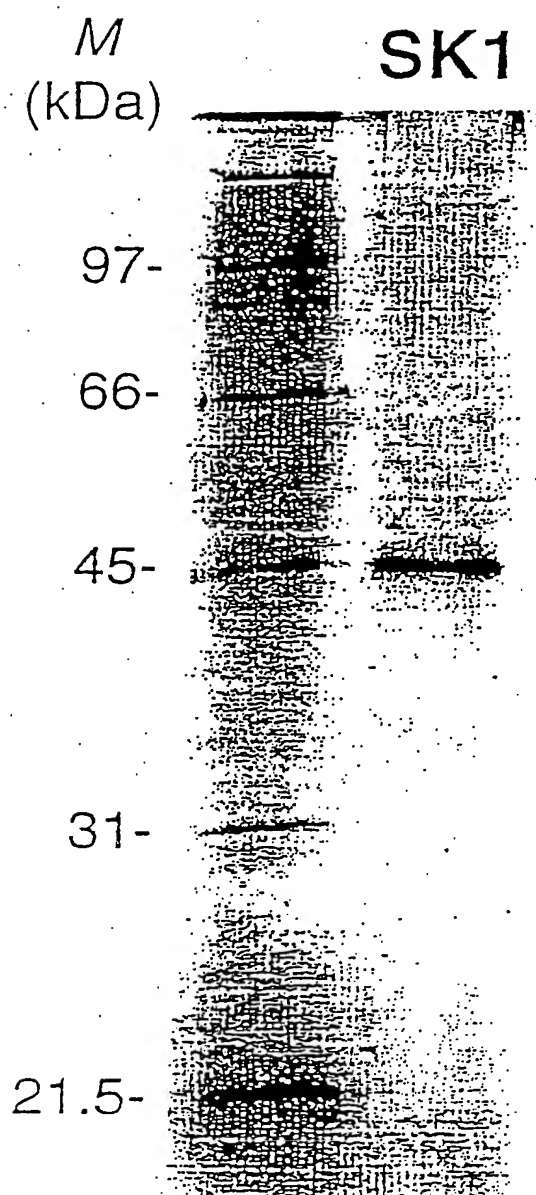


Figure 4

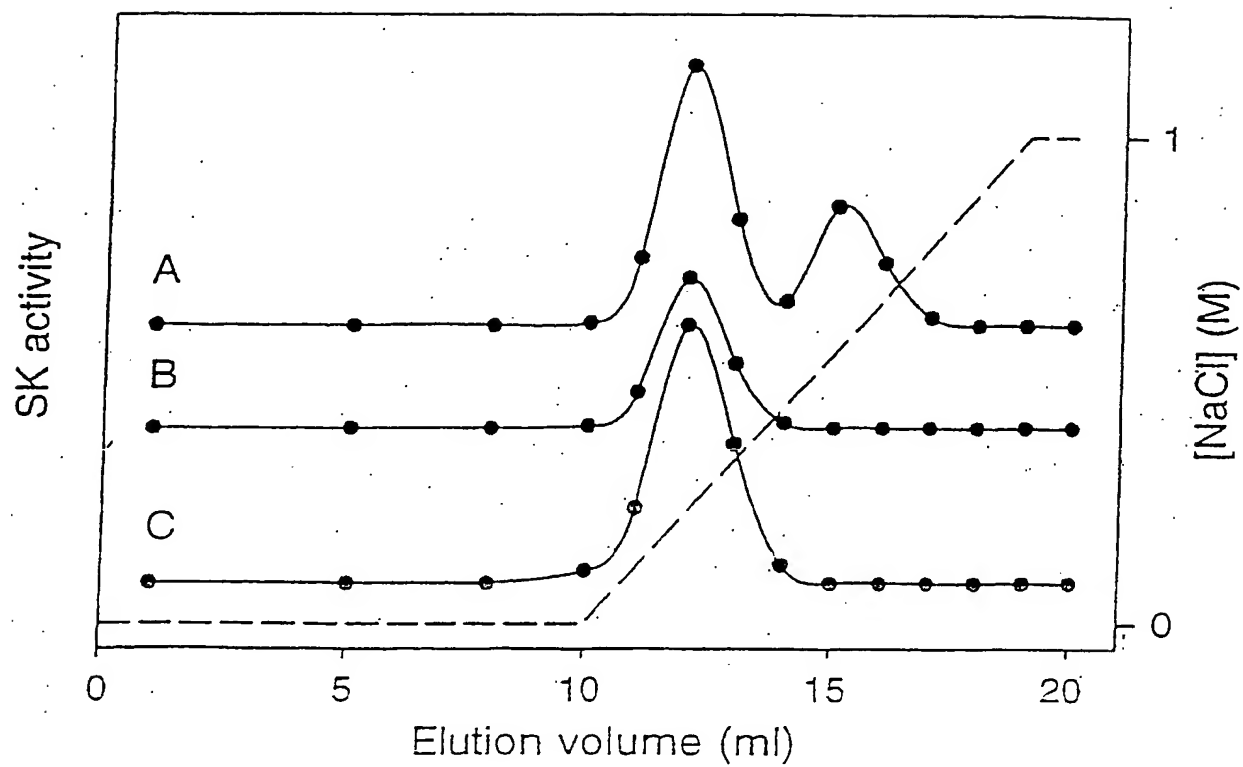


Figure 5

# Cloning of HUVEC SK

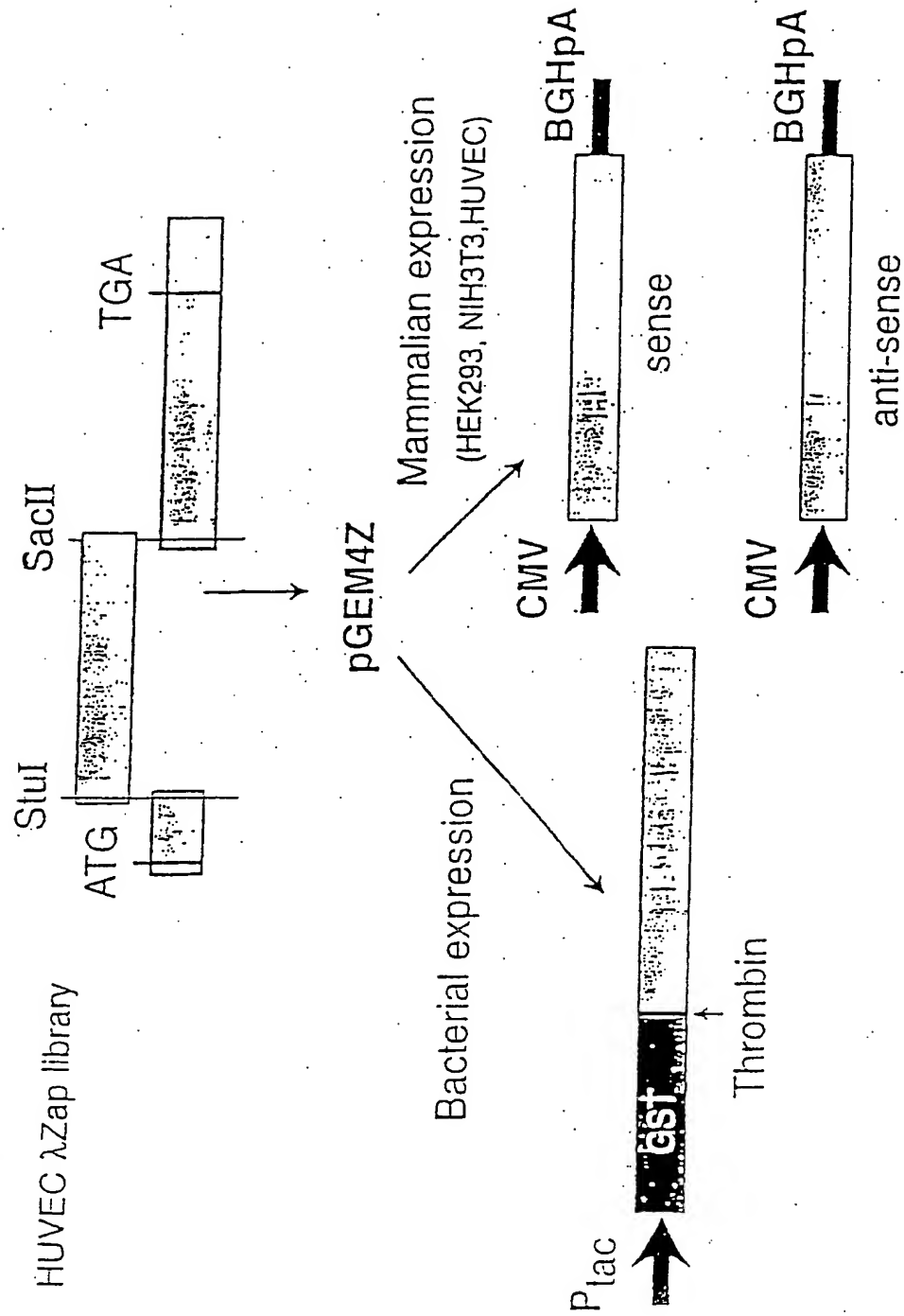


Figure 6

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1      M D P A G G P R G V L P R P C R V L V      19
1 gagccgagggtcgaggttATGGATCCAGCGGGGGCCCCCGGGGGGTGCTCCCGGGCCCTGCCCGTGGTG 75

20 L L N P R G G K A L Q L F R S H V Q P L L A E      44
76 CTGCTGAACCCGGCGGGCAAGGCAAGCCCTTGCAGCTCTTCGGAGTCACGTGCAGCCCCCTTTGGCTGAG 150

45 A E I S F T L M L T E R R N H A R E L V R S E E L      69
151 GCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGGGAAACACGCGGGAGCTGGTGGGTCCGAGGAGCTG 225

70 G R W D A L V V M S G D G L M H E V V N G L M E R      94
226 GGCCGCTGGGACGCTCTGGTTCATGTCTGGAGACGGGCTGATGCACGAGGTGGTGAACGGGCTCATGGAGCGG 300

95 P D W E T A I Q K P L C S L P A G S G N A L A A S      119
301 CCTGACTGGGAGACCGCCCATCCAGAAGCCCCCTGTGTAGCTCCACGAGGCTCTGGCAACGGCTGGCAGCTTCC 375

120 L N H Y A G Y E Q V T N E D L L T N C T L L L C R      144
376 TTGAACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCTGACCAACTGCACGCTATTGCTGTCCGC 450

145 R L L S P M N L L S L H T A S G L R L F S V L S L      169
451 CGGCTGCTCACCCATGAACCTGCTCTCTGCACACGGCTTCGGGGCTGGCCCTCTTCTCTGTGCTCAGCCTG 525

170 A W G F I A D V D L E S E K Y R R L G E M R F T L      194
526 GCCTGGGGCTTCATTGCTGATGTGGACCTAGAGAGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTG 600

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Figure 7A-1



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195 G T F L R L A A L R T Y R G R L A Y L P V G R V G 219
601 GGCAC TTCTCCTGCGTCTGGCAGCCTTGCGCACTTACCGGGCCGACTGGCTTACCTCCCTGTAGGAAGAGTGGGT 675

220 S K T P A S P V V V Q Q G P V D A H L V P L E E P 244
676 TCCAAGACACCTGCCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCCACTGGAGGAGCCA 750

245 V P S H W T V V P D E D F V L V L A L L H S H L G 269
751 GTGCCCTCTCACTGGACAGTGGTGCCCGACGAGGACTTGTGTGCTAGTCCCTGGCACTGCTGCACCTGCACCTGGGC 825

270 S E M F A A P M G R C A A G V M H L F Y V R A G V 294
826 AGTGAGATGTTTGCTGCACCCATGGGCGGCTGTGCAGCTGGCGTCATGCATCTGTTCTACGTGCGGGCGGAGTG 900

295 S R A M L L R L F L A M E K G R H M E Y E C P Y L 319
901 TCTCGTGCCATGCTGCTGCGCCTCTTCCTGGCCATGGAGAAGGCAGGCATATGGAGTATGAATGCCCTACTTG 975

320 V Y V P V V A F R L E P K D G K G M F A V D G E L 344
976 GTATATGTGCCCCGTGGTCGCCTTCCGCTTGGAGCCCCAAGGATGGGAAAGGTATGTTTGCAGTGGATGGGAATTG 1050

345 M V S E A V Q G Q V H P N Y F W M V S G C V E P P 369
1051 ATGGTTAGCGAGGCCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTGGATGGTTCAGCGGTTGCGTGGAGCCCCCG 1125

370 P S W K P Q Q M P P P E E P L 384
1126 CCCAGCTGGAAGCCCCCAGCAGATGCCACCGCCAGAGAGCCCTTatga 1173

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Figure 7A-2

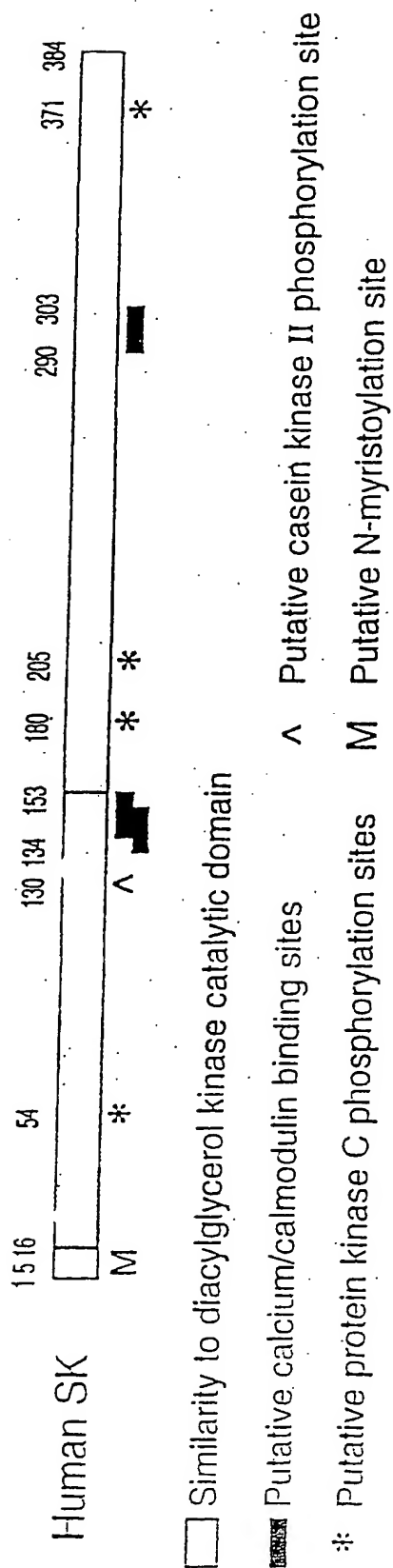
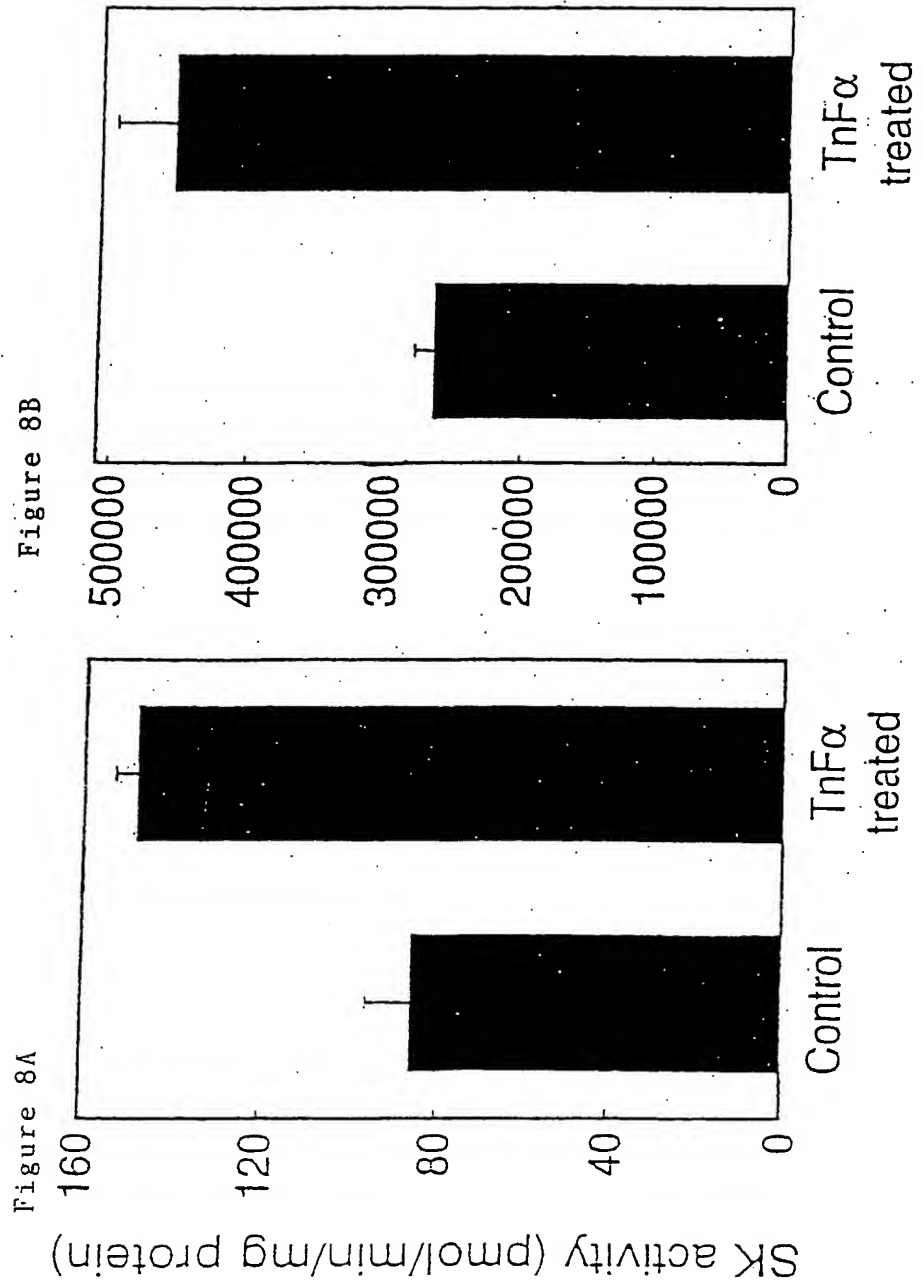


Figure 7B



hSK	1	.....MDPAGGPRGVLP	RPCRVLV	LLNPR	GGKGKALQL	FRSHVQ	PL	LAEAEIS
mSK1a	1	.....MEPECPRGLLP	PCRVLV	LLNPQ	GGKGKALQL	FQSRVQ	PF	LEAEAIT
mSK1b	1	MWCCVL	FVVECP	RGLLP	PCRVLV	LLNPQ	GGKGKALQL	FQSRVQ
Yeast LCB4	206	NISSGT	VEEILEKSYEN	SKRNR	SILV	IINPH	GGKGKALQL	FQSRVQ
Yeast LCB5	252	DL	.....VEEILKRSY	KNTRRNK	SIFV	IINPH	GGKGKAKKL	FMTKAK
S. pombe	90	.....FCEYLLD	VAYKGIK	RRR	FIV	IINPH	GGKGKAKKL	FMTKAK
C. elegans	63	ENEQLTS	VILSRKPP	PPQEQ	CRGNLL	VFINP	NSGT	GKSLET
Consensus		.....*	.....R	...*	**V	*NP	GGKGA	..*F
								..*P
								..*L
								..*
hSK	112	SGNALAAS	LNHYAGYE	QVTNED	LLTNCT	LLCRR	...	LLSPM
mSK1a	111	SGNALAAS	VNHYAGYE	QVTNED	LLINCT	LLCRR	...	RLSPM
mSK1b	118	SGNALAAS	VNHYAGYE	QVTNED	LLINCT	LLCRR	...	RLSPM
Yeast LCB4	325	SGNAM	MSIS	.....CHWTNN	PSYAA	CLVK	SIETR	IDLM
Yeast LCB5	368	SGNAM	MSVS	.....CHWTNN	PSYST	CLIK	SIETR	IDLM
S. pombe	203	SGNA	AFSYN	.....ATGQLK	PALTAL	EILK	GRPTS	FDLMT
C. elegans	184	SGNGLLC	SV	..LSKYGT	KMNEK	SVMERAL	EIATS	PTAKAES
Consensus		SGNA*	..S	.....*	L	..*	.....M	.....

Figure 9A

hSK	211	.....AYLP.....	VGRVGSKTPASPVVVQQGPVD
mSK1a	210	.....AYLP.....	VGTVASKRPAST.LVQKGPVD
mSK1b	217	.....AYLP.....	VGTVASKRPAST.LVQKGPVD
Yeast LCB4	435	ENKDKNKGCLTFEP...NPSNSSPDLLSKNNINNSTKDE.....	
Yeast LCB5	478	EH..KNKGSLEFQHITMKNKDNECDNYYENEYETENEDEDADADDEDSHLIS	
S. pombe	308	.....EKSKNLAPMSESSDSK.....	
C. elegans	284	.....TYRPHYKPGFHPSSNVFSVYEKTTQQRIDDSKVKTNGSVSDSEETME	
Consensus		.....*	
hSK	282	AGVMHLFYV..RAGVSRAMLLRLFLAMEKGRHMEYEC	PYL VYVPVVAFRLEPKDG
mSK1a	280	AGVMHLFYV..RAGVSR AALLRLFLAMQCKH MELDC	PYL VHVVPVVAFRLEPRSQ
mSK1b	287	AGVMHLFYV..RAGVSR AALLRLFLAMQCKH MELDC	PYL VHVVPVVAFRLEPRSQ
Yeast LCB4	532	DGTIDLVT DARI PVTR..MTPILLSLDKGSH..VLEPEVIH SKILAYKII	PKVE
Yeast LCB5	586	DGTMDMVT DARTSLTR..MAPILLGLDKGSH..VLQPEVLH SKILAYKII	PKLG
S. pombe	367	DGLIDVVI VYSKQFRKS..LLSMFTQLDNCGF..YYSKHLNYYK VRSFRFT	PVNT
C. elegans	388	DNRIHLSYILWKDIGTRVNIAKYLLAIEHET	LDL..PFVKHVEVSSMKLEVISE
Consensus		.G.*.....*R...*.L**..G.H.....P.*...*...*	

Figure 9B

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FTLMLTERRNNHARE.LVRSEELGRWDALVVMSCDGLMHHEVNVNGLMERPDWETAI.QKPLCSLPAG
FKLILTERKNNHARE.LVCAEELGHWDALAVMSCDGLMHHEVNVNGLMERPDWETAI.QKPLCSLPAG
FKLILTERKNNHARE.LVCAEELGHWDALAVMSCDGLMHHEVNVNGLMERPDWETAI.QKPLCSLPAG
IEIAYTKYARHAID.IAKDLDISKYDTIACASGDGIPYEIVNGLYRRPDRVDAFNKLAVTQLPCG
IEVVYTKYPGHAIE.IAREMDIDKYDTIACASGDGIPHEVINGLYQRPDHVKAFNNIAITEIPCG
CEVLTTRKDHAKS.IAKNLDVGSYDGLSVGGDGLFHEVINGLGERDDYLEAF.KLPVCMIPCG
YEVVVTTGPNHARNVLMTKADLGKFNGLVILSGDGLVFEEALNGLICREDAFRIFPTLPIGIVPSC
**T....HA.*.*.*.*.*D.*.*SGDG*.EV*NGL..R.D...A...**.*P.G

FVLSLAWGFIAADVBLESEKRYR.LGEMRFTLGTFLRLAALRTYRGRL.....
YVLSLSWGFVADVBLESEKRYR.LGEIRFTVGTFFRLASLRIYQGQL.....
YVLSLSWGFVADVBLESEKRYR.LGEIRFTVGTFFRLASLRIYQGQL.....
LSFLSQTYGVIAESDINTE.FIRWMGPVRFNLGVAFNIIOGKKYPCFVFVKYAAKSKKELKVHFL
LSFLSQTYGLIAETDINTE.FIRWMGPVRFELGVAFNIIQKKKYPCEIYVKYAAKSKNELKNHYL
YSELTANYGIIADCIDIGTE.NWRFMGENRAYLGFLLRLFQKPDWKCSIEMDVVSSDRTEIKHMY.
ASFLSIGWGLMADIDIDSEKWRKSLGHRRFTVMGFI RSCNLRSYKGRL.....
.S.LS.**G.*A*.D.**E.*.R.*G..RF.*G.....*Y.*

```

Figure 9C

AHLVPLEEPVPSHW	TVVPD	EDFVLVLALLHSHLGSEMFAA	PMGRCA	
THLVPLEEPVPSHW	TVVPE	QDFVLVLVLLHHLHLSSELFAA	PMGRCE	
THLVPLEEPVPSHW	TVVPE	QDFVLVLVLLHHLHLSSELFAA	PMGRCE	
....LSPNFLNEDNFKLYPMTEPVPRDWEKMDSELTDNLTFYTGKMPYIAKDTKFF			PAALPA	
RDLADSSADQIKEEDFKIKYPLDEGIPSDWERLDPNISNNLIGIFYTGKMPVVAADTKFF			PAALPS	
....TVSTSPESHLLTFEI		NDLSIFCAGLLPYIAPDAKMF	PAASND	
TKFQNWTLPDSDETLAVGSSDLEETVIE		DNFVNIYAVTLSHIAADGPPFA	PSAKLE	
....**	*	**	***	P
KG..MFAVDGELMVSE	AVQGVH	PNYFW.MVSGCPEPPSWKPQQMPPEEPL	identity	
RG..VFSVDGELMVCE	AVQGVH	PNYLW.MVCGSRDAPSGRDSRRGPPPEEP		81%
RG..VFSVDGELMVCE	AVQGVH	PNYLW.MVCGSRDAPSGRDSRRGPPPEEP		80%
SG..LFSVDGEEKFPLE	EPLQVEIMP	MLCKTLNRNGRYIDTEFESM		28%
NG..LFSVDGEEKFPLE	EPLQVEIMP	RLCKTLNRNGRYVDTDFDSM		30%
GKRHYFALDGE	SYPLE	PFECRVAPKLGTTLSPVAGFQLLDI		30%
GS..HVVLDGE	VVDTKTIEVASTKNHIS	VFSSTA		30%
*...F**DGE	E***	*P		*

Figure 9D

Figure 10A

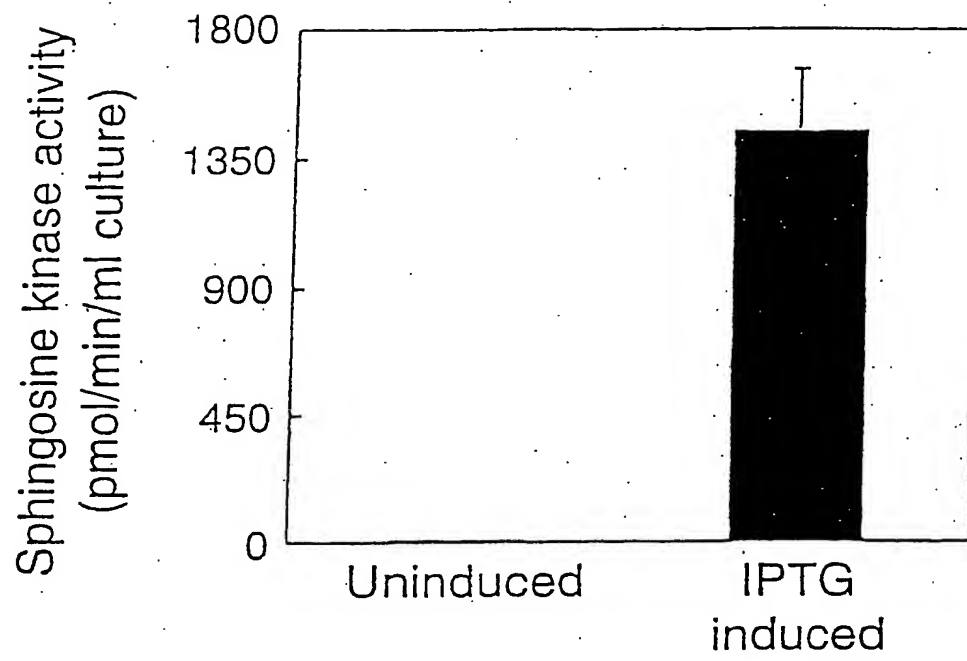


Figure 10B

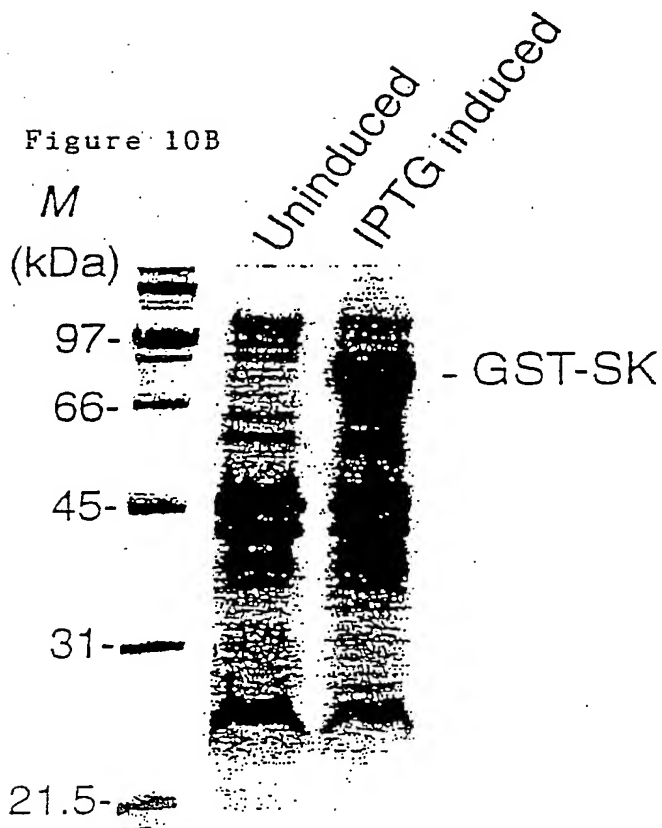
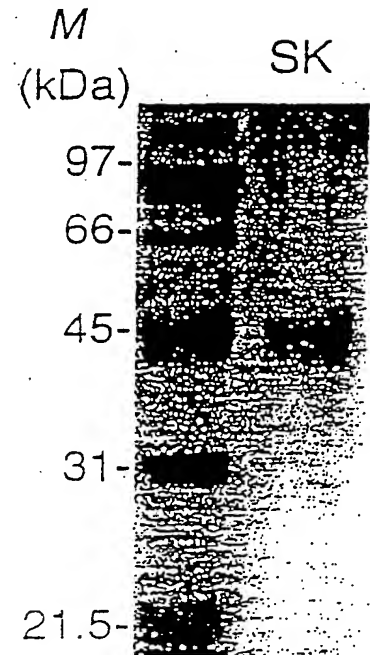


Figure 10C





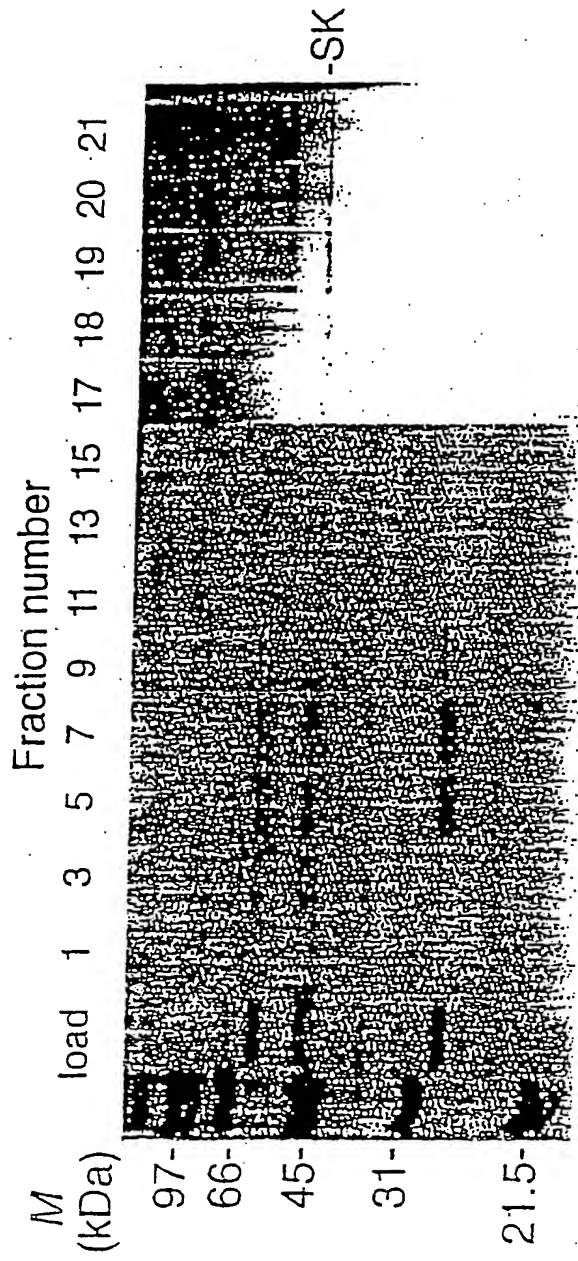


Figure 11A

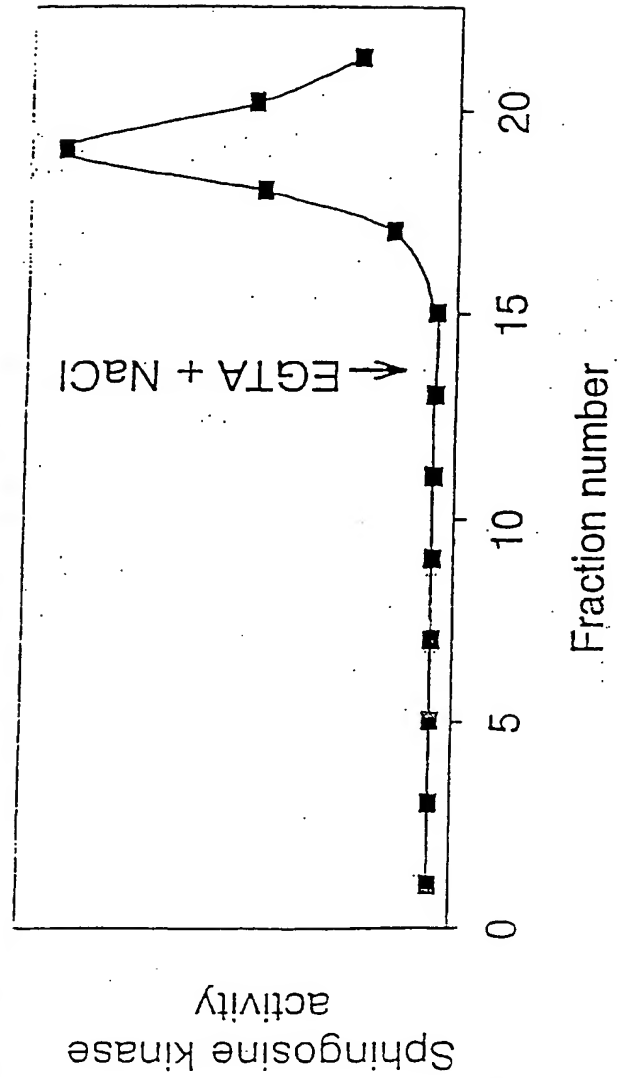


Figure 11B

Figure 12A

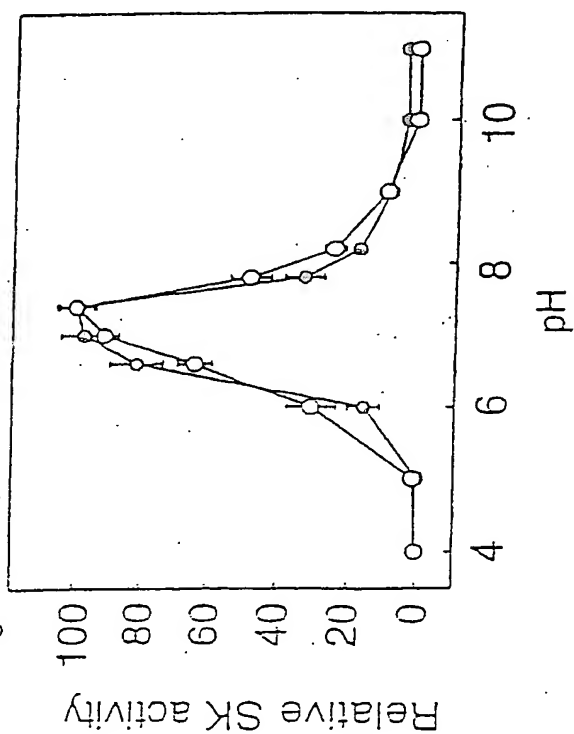


Figure 12B

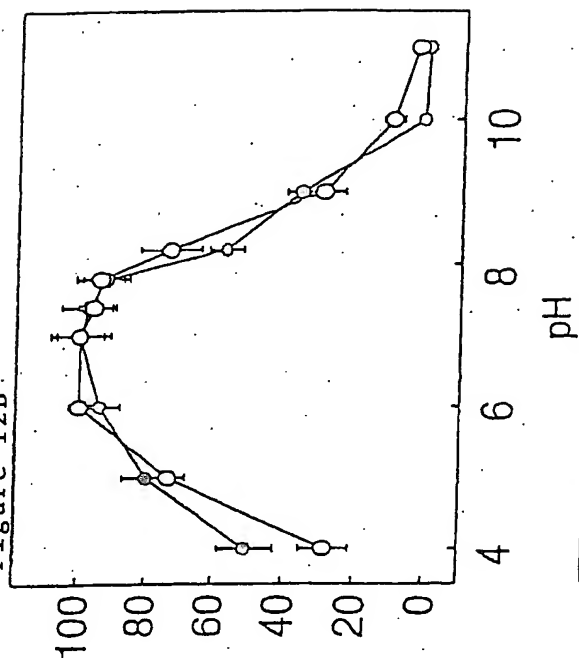


Figure 12C

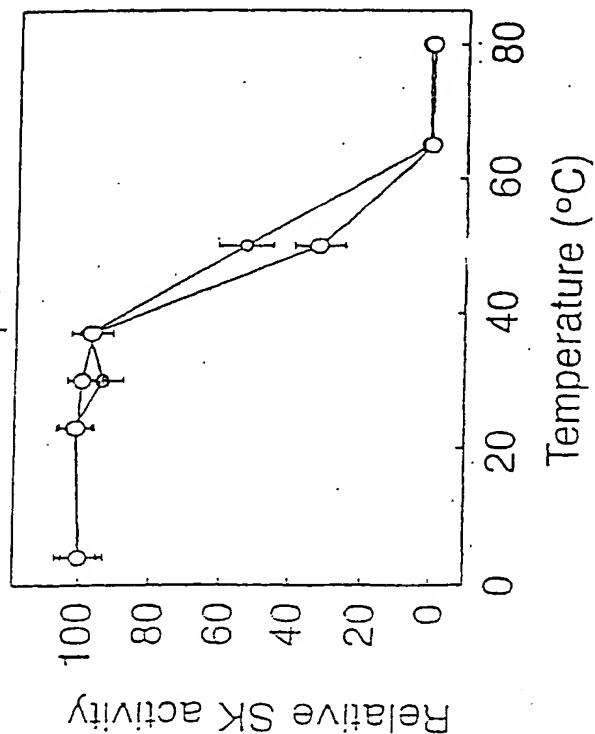
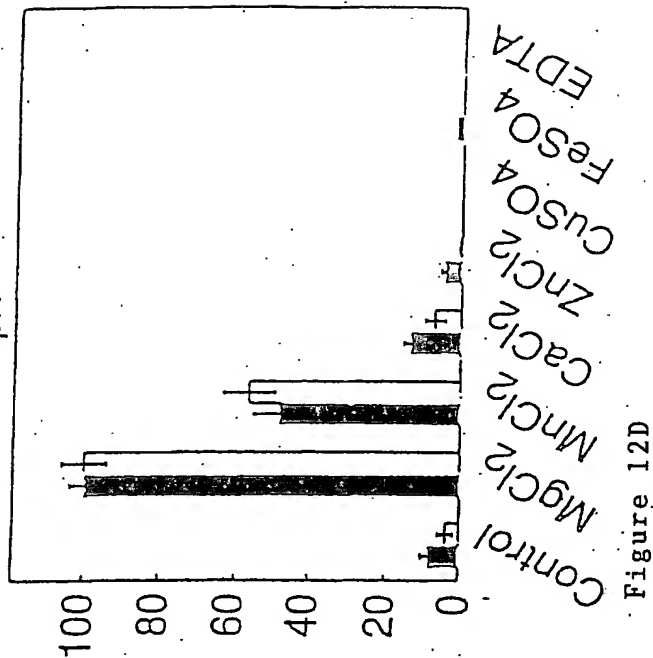
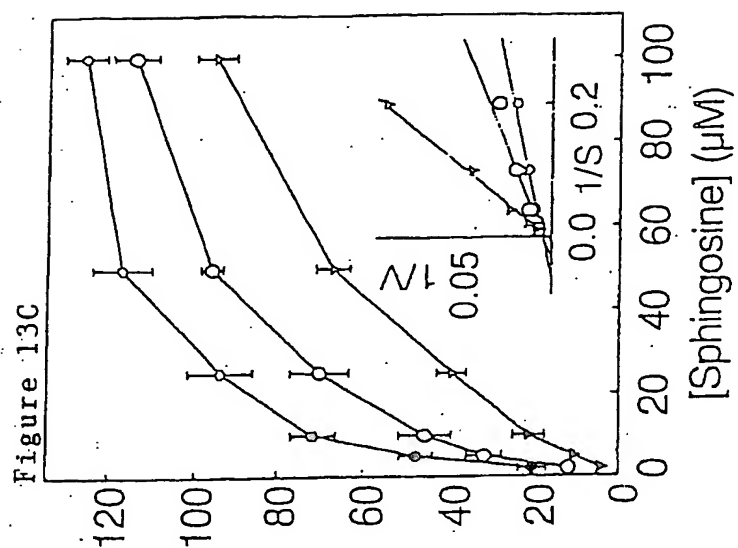
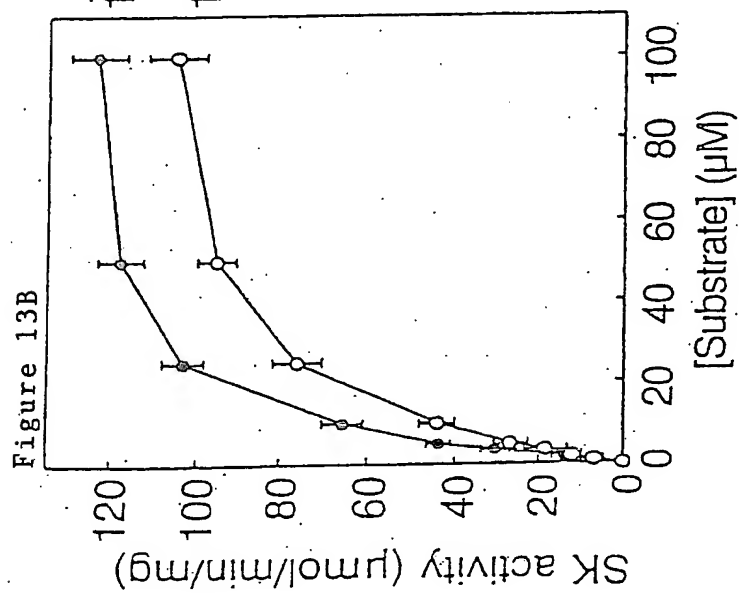
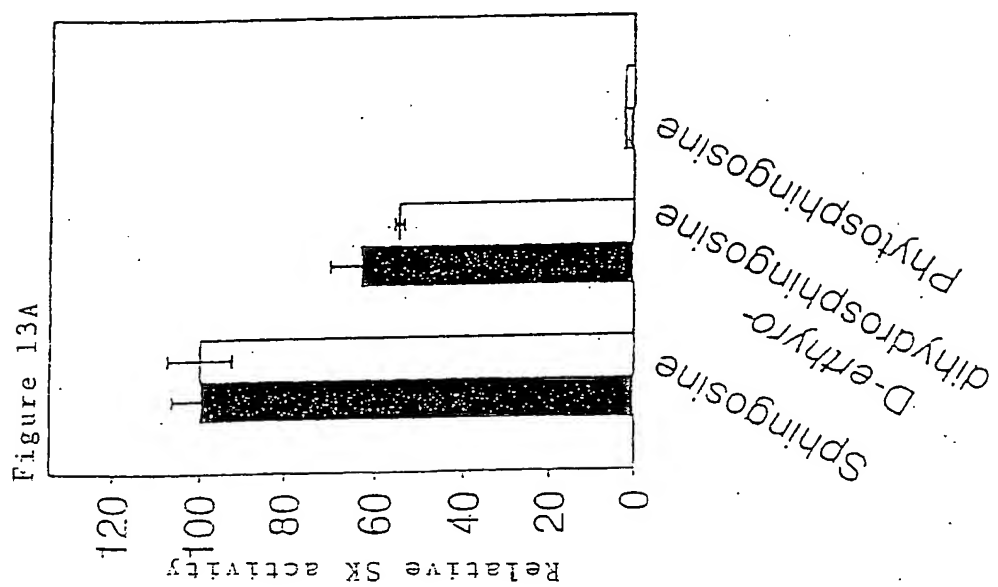


Figure 12D





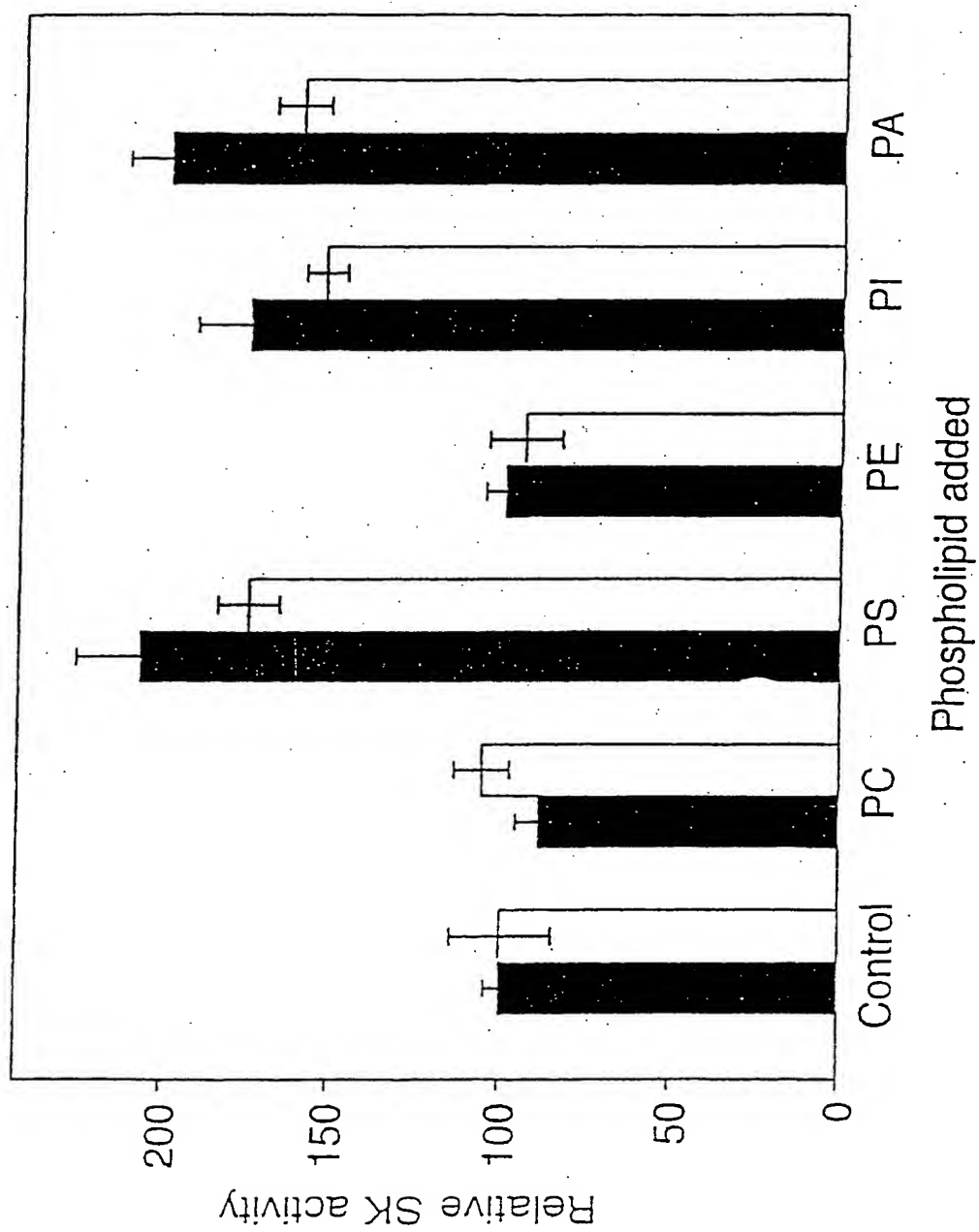


Figure 14